Reviewed, UniProtKB/Swiss-Prot P35327 (LUXS_VIBF1) Last modified December 15, 2009, Version 63.

Names	and	oriain
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Protein names	Recommended name: Transcriptional activator protein luxR		
Gene names	Name: luxR Ordered Locus Names: VF_A0925		
Organism	Vibrio fischeri (strain ATCC 700601 / ES114) [Complete proteome] [HAMAP]		
Taxonomic identifier	312309 [NCBI]		
Taxonomic lineage	Bacteria · Proteobacteria · Gammaproteobacteria · Vibrionales · Vibrionaceae · Aliivibrio		

Protein attributes

Sequence length	250 AA.
Sequence status	Complete.
Sequence processing	The displayed sequence is not processed.
Protein existence	Inferred from homology.

General annotation (Comments)

Function	Transcriptional activator of the bioluminescence operon. Binds to the OHHL autoinducer.		
Sequence similarities	Belongs to the autoinducer-regulated transcriptional regulatory protein family. Contains 1 HTH luxR-type DNA-binding domain.		

Ontologies

Keywords

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Biological process	Luminescence	
	Quorum sensing	
	Transcription	
	Transcription regulation	

Ligand	DNA-binding			
Molecular function	Activator			
Technical term	Complete proteome			
Gene Ontology (GO)				
Biological process	bioluminescence Inferred from electronic annotation Source: UniProtK8-KW			
	quorum sensing Inferred from electronic annotation, Source: UniProtKB-KW			
	regulation of transcription, DNA-dependent Inferred from electronic annotation. Source: InterPro			
	transcription Inferred from electronic annotation, Source: UniProtKB-KW			
	two-component signal transduction system (phosphorelay) Inferred from electronic annotation. Source, InterPro			
Cellular component	intracellular Inferred from electronic annotation. Source: InterPro			
Molecular function	sequence-specific DNA binding Interned from electronic annotation. Source: InterPro			
	transcription factor activity Inferred from electronic annotation. Source: InterPro			
	two-component response regulator activity inferred from electronic annotation. Source: InterPro			

Complete GO annotation...

Sequence annotation (Features)

Feature key	(s)	Length	Description Graphical view		i
Molecule processing					
☐ Chain	1 – 250	250	Transcriptional activator protein luxR		F
Regions					
□ Domain	176 – 241	66	HTH luxR-type	- 1	

	DNA binding	200 – 219	20	H-T-H motif	11
m	Compositional bias	11 – 20	10	Arg/Lys-rich (basic)	П
П	Compositional bias	64 – 67	4	Arg/Lys-rich (basic)	ı
	Compositional bias	104 – 114	11	Lys-rich (basic)	П

Sequences

Sequence				Lenç	gth Mass (Da)
P35327-1 [Un	iParc].				
Last modified I	February 1, 1	994. Version	FASTA	2	50 28,520
Checksum: 42	AC06375E28	BA34F			
10	20	30	40	50	60
		NNKDINQCLS			
7 <u>0</u>	8 <u>0</u>	9 <u>0</u>	10 <u>0</u>	11 <u>0</u>	12 <u>0</u>
		VVDYSKSHHS			KEAQESGLIT
13 <u>0</u>	140	15 <u>0</u>	16 <u>0</u>	17 <u>0</u>	18 <u>0</u>
GFSFPIHTAS	NGFGMLSFAH	SDKDIYTDSL	FLHASTNVPL	MLPSLVDNYQ	KINTTRKKSD
190	200	210	220	230	240
SILTKREKEC	LAWASEGKST	WDISKILGCS	ERTVTFHLTN	TQMKLNTTNR	CQSISKAILT
25 <u>0</u> GAINCPYLKN					

« Hide

References

« Hide 'large scale' references

"Sequencing and analysis of luxR and luxl, the luminescence regulatory genes from the squid light organ symbiont Vibrio fischeri ES114."

[1] Gray K.M., Greenberg E.P.

Mol. Mar. Biol. Biotechnol. 1:414-419(1992)
Cited for: NUCLEOTIDE SEQUENCE [GENOMIC DNA].

[&]quot;Complete genome sequence of Vibrio fischeri: a symbiotic bacterium with

pathogenic congeners."

Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R., Lostroh P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E., Stevens A., Visick K.,

[2] Whistler C., Greenberg E.P.

Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005) [PubMed: 15703294]

[Abstract]

Cited for: NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Cross-references

Sequence databases

EMBL •	M96844 Genomic DNA. Translation: AAA27542.1.
	CD000021 Conomic DNA Translation: AAM/97005

RefSea YP 206883.1.

3D structure databases

ModBase Search...

Protein-protein interaction databases

STRING P35327.

Genome annotation databases

GeneID 3280300.

GenomeReviews Gene locus VF A0925 in contig CP000021 GR.

KEGG vfi:VF A0925.

NMPDR fig|312309.3.peg.3316.

Organism-specific databases

CMR Search...

Phylogenomic databases

HOGENOM HBG303913.

OMA ITIRERE

Enzyme and pathway databases

BioCyc VFIS312309:VFA0925-MON.

Family and domain databases

InterPro IPR005143. Autoind bd.

	IPR016032. Sig_transdc_resp-reg_C-effctor. IPR000792. Tscrpt_reg_LuxR_C. IPR011991. Wing_hlx_DNA_bd. [Graphical view]
Gene3D	G3DSA:1.10.10.10. Wing_hlx_DNA_bd. 1 hit.
Pfam	PF03472. Autoind_bind. 1 hit. PF00196. GerE. 1 hit. [Graphical view]
PRINTS	PR00038. HTHLUXR.
SMART	SM00421. HTH_LUXR. 1 hit. [Graphical view]
PROSITE	PS00622. HTH_LUXR_1. 1 hit. PS50043. HTH_LUXR_2. 1 hit. [Graphical view]
ProtoNet	Search

Entry information

Entry name	LUXS_VIBF1		
Accession	Primary (citable) accession number: P35327 Secondary accession number(s): Q5DZ01		
Entry history	Integrated into UniProtKB/Swiss-February 1, 1994 Prot: Last sequence update: Last modified: December 15, 2009 This is version 63 of the entry and version 1 of the sequence. [Complete history]		
Entry status	Reviewed (UniProtKB/Swiss-Prot)		
Annotation project	HAMAP (High-quality Automated and Manual Annotation of microbial Proteomes)		

Relevant documents

SIMILARITY comments

Index of protein domains and families







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